1: Nat Biotechnol. 2000 Nov;18(11):1185-90.

Related Articles, Links

nature biotechnology

Entrez PubMed

Enhancement of tumor necrosis factor alpha antitumor immunotherapeutic properties by targeted delivery to aminopeptidase N (CD13).

Curnis F, Sacchi A, Borgna L, Magni F, Gasparri A, Corti A.

Department of Biological and Technological Research, San Raffaele H Scientific Institute, via Olgettina 58, 20132 Milan, Italy.

PubMed Services

The clinical use of tumor necrosis factor alpha (TNF) as an anticancer drug is limited to local treatments because of its dose-limiting systemic toxicity. We show here that murine TNF fused with CNGRC peptide (NGR-TNF), an aminopeptidase N (CD13) ligand that targets activated blood vessels in tumors, is 12-15 times more efficient than murine TNF in decreasing the tumor burden in lymphoma and melanoma animal models, whereas its toxicity is similar. Similarly, human NGR-TNF induced stronger antitumor effects than human TNF, even with 30 times lower doses. Coadministration of murine NGR-TNF with a CNGRC peptide or an anti-CD13 antibody markedly decreased its antitumor effects. Tumor regression, induced by doses of murine NGR-TNF lower than the LD50, was accompanied by protective immunity. In contrast, no cure was induced by TNF at any dose. These results suggest that targeted delivery of TNF to CD13 may enhance its immunotherapeutic properties. Moreover, these findings reveal the potential of tumor homing peptides to generate a new class of recombinant cytokines that compared to immunocytokines have a simpler structure, could be easier to produce and are potentially less immunogenic.

Related Resources

PMID: 11062439 [PubMed]

1: J Immunother. 1991 Apr;10(2):105-11. Related Articles, Links

Entrez PubMed

Antitumor activity of a novel chimera tumor necrosis factor (TNF-STH) constructed by connecting rTNF-S with thymosin beta 4 against murine syngeneic tumors.

Noguchi K, Inagawa H, Tsuji Y, Morikawa A, Mizuno D, Soma G.

Biotechnology Research Center, Teikyo University, Kanagawa, Japan.

PubMed Services

We have shown the in vivo usefulness of a novel chimera tumor necrosis factor (TNF), called rTNF-STH, which was constituted with human thymosin beta 4 and recombinant human TNF-SAM1. Tumor necrosis was induced by intravenous injection of a smaller amount of rTNF-STH (1 x 10(3) U/mouse, 0.67 microgram/mouse) than rTNF-alpha or rTNF-S (1 x 10(4) U/mouse, 2.5-5 micrograms/mouse). Significant antitumor effects of rTNF-STH to Meth A fibrosarcoma, B16 melanoma, MH134 hepatoma, or Lewis lung carcinoma (3LL) were observed by systemic injection of rTNF-STH at the maximum tolerable dose of 1 x 10(4) U/mouse (6.7 micrograms/mouse); this dose did not cause regression of tumors by conventional rTNF-alpha. rTNF-STH showed a significant prolongation of its half-life in serum. The average calculated half-life of the chimera protein is about 110 min, which is 15 times longer than that of original TNF-SAM1 (7.5 min). On the basis of this prolongation of half-life of rTNF-STH and its efficient hemorrhagic necrotic activity, the antitumor effect of rTNF-STH--as compared with that of the known TNF species--is discussed. Findings indicate that use of the chimera protein to alter the N-terminal region of TNF may be a promising approach to obtain molecules that more favorably attack tumors and other diseases than conventional rTNFs.

PMID: 2043590 [PubMed]

Related Resources

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 06:25:25 ; Search time 194.56 Seconds
(without alignments)
11.413 Million cell updates/sec

Title: US-10-046-922-68
Perfect score: 39
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62XX
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	100.0	8	13	US-10-046-922-68	Sequence 68, Appl
2	39	100.0	10	13	US-10-046-922-73	Sequence 73, Appl
3	38	97.4	7	13	US-10-046-922-67	Sequence 67, Appl
4	27	69.2	11	9	US-09-813-653-23	Sequence 23, Appl
5	26	66.7	6	16	US-10-664-021-68	Sequence 68, Appl
6	26	66.7	7	16	US-10-664-021-67	Sequence 67, Appl
7	26	66.7	7	16	US-10-664-021-80	Sequence 80, Appl
8	26	66.7	8	14	US-10-351-641-1668	Sequence 1668, Ap
9	26	66.7	8	15	US-10-462-262-235	Sequence 235, App
10	26	66.7	8	16	US-10-664-021-62	Sequence 62, Appl
11	26	66.7	84	12	US-10-424-599-157766	Sequence 157766,
12	25	64.1	5	16	US-10-664-021-69	Sequence 69, Appl
13	25	64.1	6	16	US-10-664-021-79	Sequence 79, Appl
14	25	64.1	7	16	US-10-664-021-78	Sequence 78, Appl
15	25	64.1	8	16	US-10-664-021-74	Sequence 74, Appl
16	25	64.1	29	9	US-09-925-299-1401	Sequence 1401, Ap
17	25	64.1	29	10	US-09-925-299-1401	Sequence 1401, Ap
18	25	64.1	49	12	US-10-424-599-191303	Sequence 191303,
19	25	64.1	51	12	US-10-424-599-267294	Sequence 267294,
20	25	64.1	90	9	US-09-939-980-262	Sequence 262, App
21	25	64.1	91	12	US-10-424-599-202397	Sequence 202397,
22	25	64.1	108	12	US-10-424-599-226458	Sequence 226458,
23	25	64.1	130	14	US-10-106-698-7251	Sequence 7251, Ap
24	25	64.1	211	12	US-10-424-599-251390	Sequence 251390,
25	25	64.1	214	14	US-10-259-165-28	Sequence 28, Appl
26	25	64.1	214	14	US-10-259-165-374	Sequence 374, App
27	25	64.1	229	12	US-09-925-298-554	Sequence 554, App
28	25	64.1	229	14	US-10-102-806-554	Sequence 554, App
29	25	64.1	236	15	US-10-264-049-4279	Sequence 4279, Ap
30	25	64.1	791	12	US-10-282-122A-46607	Sequence 46607, A
31	24.5	62.8	94	12	US-10-424-599-285625	Sequence 285625,
32	24	61.5	5	12	US-10-436-549-496	Sequence 496, App
33	24	61.5	5	12	US-10-436-549-525	Sequence 525, App
34	24	61.5	7	9	US-09-884-767A-38	Sequence 38, Appl
35	24	61.5	7	10	US-09-563-222-53	Sequence 53, Appl
36	24	61.5	7	16	US-10-403-938-27	Sequence 27, Appl
37	24	61.5	8	12	US-10-367-580-267	Sequence 267, App
38	24	61.5	8	12	US-10-367-593-267	Sequence 267, App
39	24	61.5	8	12	US-10-367-594-267	Sequence 267, App
40	24	61.5	8	12	US-10-367-654-267	Sequence 267, App
41	24	61.5	8	12	US-10-367-658-267	Sequence 267, App
42	24	61.5	8	12	US-10-367-668-267	Sequence 267, App
43	24	61.5	8	14	US-10-050-902-179	Sequence 179, App
44	24	61.5	8	14	US-10-050-902-180	Sequence 180, App
45	24	61.5	8	14	US-10-050-898-179	Sequence 179, App

ALIGNMENTS

RESULT 1
US-10-046-922-68
; Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68

Query Match 100.0%; Score 39; DB 13; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWXXXWX 8
||||||||
Db 1 GYWXXXWX 8

RESULT 2
US-10-046-922-73

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; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, Kari
;  APPLICANT:  Koivunen, Erkki
;  APPLICANT:  Kubo, Hajime
;  TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
;  FILE REFERENCE: 28967/37084A
;  CURRENT APPLICATION NUMBER: US/10/046,922
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: peptide library
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (5)..(7)
;   OTHER INFORMATION: X is any amino acid
;   NAME/KEY: SITE
;   LOCATION: (9)..(9)
;   OTHER INFORMATION: X is any amino acid
US-10-046-922-73

  Query Match             100.0%;  Score 39;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 1.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYWXXXWX 8
              ||||||||
Db          2 GYWXXXWX 9


RESULT 3
US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, Kari
;  APPLICANT:  Koivunen, Erkki
;  APPLICANT:  Kubo, Hajime
;  TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
;  FILE REFERENCE: 28967/37084A
;  CURRENT APPLICATION NUMBER: US/10/046,922
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: peptide
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (4)..(6)
;   OTHER INFORMATION: X at position 4-6 is any amino acid
US-10-046-922-67

  Query Match             97.4%;  Score 38;  DB 13;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYWXXXW 7
              |||||||
Db          1 GYWXXXW 7


RESULT 4
US-09-813-653-23
; Sequence 23, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
;  APPLICANT: Nestor, John
;  APPLICANT:  Wilson, Carol
;  APPLICANT:  See, Raymond
;  APPLICANT:  Tan Hehir, Christina
;  TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compou
;  FILE REFERENCE: CNS-005
;  CURRENT APPLICATION NUMBER: US/09/813,653
;  CURRENT FILING DATE:  2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/190,946
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/190,996
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: US 60/191,299
;  PRIOR FILING DATE: 2000-03-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: exemplary library CPI-10042
;   NAME/KEY: MOD_RES
;   LOCATION: (11)..(11)
;   OTHER INFORMATION: AMIDATION
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(11)
;   OTHER INFORMATION: wherein each Xaa represents an amino acid
US-09-813-653-23

  Query Match             69.2%;  Score 27;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GYWXXX 6
              ||||||
Db          6 GYWXXX 11


RESULT 5
US-10-664-021-68
; Sequence 68, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, an
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-68

  Query Match             66.7%;  Score 26;  DB 16;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          3 WXXXWX 8
              ||||||
Db          1 WXXXWX 6


RESULT 6
US-10-664-021-67
; Sequence 67, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-67

  Query Match             66.7%;  Score 26;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db          1 WXXXWX 6


RESULT 7
US-10-664-021-80
; Sequence 80, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(7)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-80

  Query Match             66.7%;  Score 26;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db          1 WXXXWX 6


RESULT 8
US-10-351-641-1668
; Sequence 1668, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
;  APPLICANT: Barney, S.
;  APPLICANT:  Guthrie, K.
;  APPLICANT:  Merutka, G.
;  APPLICANT:  Anwer, M.
;  APPLICANT:  Lambert, D.
;  TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;  TITLE OF INVENTION:  PROPERTIES
;  FILE REFERENCE: 7872-100
;  CURRENT APPLICATION NUMBER: US/10/351,641
;  CURRENT FILING DATE:  2003-01-24
;  PRIOR APPLICATION NUMBER: 09/350,641
;  PRIOR FILING DATE: 1999-07-09
;  PRIOR APPLICATION NUMBER: 09/315,304
;  PRIOR FILING DATE: 1999-05-20
;  PRIOR APPLICATION NUMBER: 09/082,279
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 1757
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1668
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: HIV-1
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (1)...(8)
;   OTHER INFORMATION: Xaa=unknown amino acid
US-10-351-641-1668

  Query Match             66.7%;  Score 26;  DB 14;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db          1 WXXXWX 6


RESULT 9
US-10-462-262-235
; Sequence 235, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
;  APPLICANT: Sato, Aaron K.
;  APPLICANT:  Dawson, Bruce M.
;  TITLE OF INVENTION: PROTEIN ANALYSIS
;  FILE REFERENCE: 10280-052001
;  CURRENT APPLICATION NUMBER: US/10/462,262
;  CURRENT FILING DATE:  2003-06-16
;  PRIOR APPLICATION NUMBER: US 60/388,642
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 430
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 235
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;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: exemplary motif
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 1
;   OTHER INFORMATION: Xaa = Z1 = one amino acid or is absent
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 2
;   OTHER INFORMATION: Xaa = Phe or Tyr
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 4
;   OTHER INFORMATION: Xaa = Z2 = Ala, Cys, Phe, Lys, Pro, Arg, Trp, or
;   OTHER INFORMATION: Tyr
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 5
;   OTHER INFORMATION: Xaa = Z2 = Cys, Asp, Glu, Gly, His, Lys,
;   OTHER INFORMATION: Met,Asn,Gln, Arg, Ser, Thr, Val, or Tyr
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 6
;   OTHER INFORMATION: Xaa = Z2 = Ala,Glu, Phe, His, Ile, Lys, Leu, Gln,
;   OTHER INFORMATION: Arg, Ser, Thr, Val, or Tyr
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (8)...(0)
;   OTHER INFORMATION: Xaa =  Z3 =at least one amino acid
US-10-462-262-235

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  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db          3 WXXXWX 8


RESULT 10
US-10-664-021-62
; Sequence 62, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8)..(8)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-62

  Query Match             66.7%;  Score 26;  DB 16;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db          1 WXXXWX 6


RESULT 11
US-10-424-599-157766
; Sequence 157766, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated W
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 157766
;   LENGTH: 84
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(84)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_113482C.1.pep
US-10-424-599-157766

  Query Match             66.7%;  Score 26;  DB 12;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXWX 8
              ||||||
Db         65 WXXXWX 70


RESULT 12
US-10-664-021-69
; Sequence 69, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, a
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 69
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
```

```
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(4)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-69

  Query Match             64.1%;  Score 25;  DB 16;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXW 7
              |||||
Db          1 WXXXW 5


RESULT 13
US-10-664-021-79
; Sequence 79, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
;   LENGTH: 6
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3)..(5)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-79

  Query Match             64.1%;  Score 25;  DB 16;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXW 7
              |||||
Db          2 WXXXW 6


RESULT 14
US-10-664-021-78
; Sequence 78, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; Xaa is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2)..(2)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-78

  Query Match             64.1%;  Score 25;  DB 16;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXW 7
              |||||
Db          3 WXXXW 7


RESULT 15
US-10-664-021-74
; Sequence 74, Application US/10664021
; Publication No. US20040076637A1
; GENERAL INFORMATION:
;  APPLICANT: Trimeris, Inc.
;  TITLE OF INVENTION: HIV-Derived HR1 Peptides Modified to Form Stable Trimers, and
;  TITLE OF INVENTION:  Their Use In Therapy to Inhibit Transmission of Human
;  TITLE OF INVENTION:  Immunodeficiency Virus
;  FILE REFERENCE: TRM-001
;  CURRENT APPLICATION NUMBER: US/10/664,021
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: US 60/414,514
;  PRIOR FILING DATE: 2002-09-27
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthesized; X is any amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(1)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3)..(3)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (5)..(7)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-664-021-74

  Query Match             64.1%;  Score 25;  DB 16;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WXXXW 7
              |||||
Db          4 WXXXW 8


Search completed: May  7, 2004, 06:48:23
Job time : 195.56 secs
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CC modulating fusogenic events and intracellular processes involving coiled-
CC coil peptide interactions. Other uses include preventing, treating and/or
CC diagnosing disorders involving fusion events (e.g. modulation of
CC neurotransmitter exchange and sperm-egg fusion), intracellular processes
CC involving coiled-coil peptides (e.g. bacterial infections) and viral
CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral
CC infections caused by human immunodeficiency virus, respiratory syncytial
CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and
CC polio virus). The enhancer peptide sequence increases the half-life and
CC reduces the clearance rate of therapeutic peptides, which increases their
CC efficacy and minimises the incidence and severity of adverse side
CC effects. In addition, this increases the sensitivity of the diagnostic
CC procedure in which they are used. (Updated on 06-AUG-2003 to correct OS
CC field.) (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 8 AA;

Query Match 66.7%; Score 26; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 1 WXXXWX 6

RESULT 10
ABU57814
ID ABU57814 standard; protein; 46 AA.
XX
AC ABU57814;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 polypeptide #10.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KW envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US20021S1473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
PA (JUDI/) JUDICE J K.
PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.
XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Fig 23B; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41 peptide used in the creation of the locked helix
CC peptides of the invention
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

RESULT 11
ABU57816
ID ABU57816 standard; protein; 46 AA.
XX
AC ABU57816;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 polypeptide #12.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KW envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
PA (JUDI/) JUDICE J K.
PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.

XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Fig 23B; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41 peptide used in the creation of the locked helix
CC peptides of the invention
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

RESULT 12
ABU57818
ID ABU57818 standard; peptide; 46 AA.
XX
AC ABU57818;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 associated locked helix peptide #2.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41.
XX
OS Synthetic.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
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PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.
XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Page 36; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of a HIV gp41
CC derived locked-helix polypeptide
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

RESULT 13
ABU57810
ID ABU57810 standard; protein; 46 AA.
XX
AC ABU57810;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 polypeptide #6.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KW envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX

PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
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PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.
XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Fig 23A; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41 peptide used in the creation of the locked helix
CC peptides of the invention
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

RESULT 14
ABU57811
ID ABU57811 standard; protein; 46 AA.
XX
AC ABU57811;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 polypeptide #7.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KW envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
PA (JUDI/) JUDICE J K.
PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.
XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Fig 23A; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41 peptide used in the creation of the locked helix
CC peptides of the invention
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

RESULT 15
ABU57807
ID ABU57807 standard; protein; 46 AA.
XX

AC ABU57807;
XX
DT 10-APR-2003 (first entry)
XX
DE HIV envelope protein gp41 polypeptide #3.
XX
KW Human immunodeficiency virus; HIV; vaccine; helical peptide compound;
KW viral membrane fusion; hapten; immunogen; peptidomimetic; gp41;
KW envelope protein.
XX
OS Human immunodeficiency virus.
XX
PN US2002151473-A1.
XX
PD 17-OCT-2002.
XX
PF 15-MAY-2001; 2001US-00854816.
XX
PR 06-NOV-1996; 96US-00743698.
PR 16-JUN-1997; 97US-0049787P.
PR 16-JUN-1997; 97US-00876698.
PR 05-NOV-1997; 97US-00965056.
XX
PA (BRAI/) BRAISTED A C.
PA (JUDI/) JUDICE J K.
PA (MCDO/) MCDOWELL R S.
PA (PHEL/) PHELAN J C.
PA (STAR/) STAROVASNIK M A.
PA (WELL/) WELLS J A.
XX
PI Braisted AC, Judice JK, Mcdowell RS, Phelan JC, Starovasnik MA;
PI Wells JA;
XX
DR WPI; 2003-182525/18.
XX
PT Novel constrained helical peptide compound useful for prophylactically or
PT therapeutically treating mammal at risk for or infected with human
PT immunodeficiency virus.
XX
PS Disclosure; Fig 23A; 180pp; English.
XX
CC The invention describes a constrained helical peptide compound (I)
CC comprising a first constrained helical peptide comprising a sequence of 8
CC amino acids (a.as) having a first and second terminal residue both
CC flanking an internal sequence of 6 a.as, where the terminal residues have
CC a side chain that are linked to each other forming a locking group to
CC form a constrained helical peptide. (I) is useful for preparing
CC antibodies that prevent viral membrane fusion, as haptens, preferably
CC attached to a carrier, for use as an immunogen to raise antibodies that
CC have a diagnostic use, as a vaccine for treatment of patients at risk of
CC or infected with HIV, to create combinatorial constrained helical peptide
CC libraries that are useful in chemical selection systems, to isolate the
CC binding determinants from alpha-helical binding domains of known
CC proteins, for determining whether a binding determinate in an alpha-
CC helical binding domain of a known protein can serve as a structural model
CC for the design of peptidomimetics, to replace intact binding proteins or
CC protein binding domains in the affinity purification of ligands, to mimic
CC epitopes in proteins to selectively raise polyclonal or monoclonal
CC antibodies against such individual epitopes for isolating synthetic
CC antibody clones with a selected binding activity from phage display
CC combinatorial libraries, to provide conformationally stable variants of
CC peptides or proteins which exhibit floppy or unstable alpha-helical
CC secondary structure at one or more sites in unrestrained form under
CC conditions of interest. This is the amino acid sequence of an HIV
CC envelope protein gp41 peptide used in the creation of the locked helix
CC peptides of the invention
XX
SQ Sequence 46 AA;

Query Match 66.7%; Score 26; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WXXXWX 8
||||||
Db 39 WXXXWX 44

Search completed: May 7, 2004, 06:27:57
Job time : 45.76 secs